

**BEST AVAILABLE COPY**

The following listing of claims will replace all prior versions, and listings, of claims in this application:

Claims 1-45 (Cancelled).

46. (New) A process for preparing L-amino acids, comprising:  
culturing a recombinant modified Coryneform bacterium for a time and under  
conditions suitable for producing L-amino acids, and  
collecting the L-amino acids;  
wherein the recombinant modified Coryneform bacterium expresses a reduced level  
of the otsA gene product, which is a trehalose 6-phosphate synthase, compared to an  
unmodified Coryneform bacterium, or  
wherein the recombinant modified Coryneform bacterium expresses a otsA gene  
product having reduced trehalose 6-phosphate synthase activity compared to the otsA gene  
product expressed in an unmodified Coryneform bacterium.

47. (New) The process of Claim 46, wherein the recombinant modified Coryneform  
bacterium expresses a reduced level of the otsA gene product, which is a trehalose 6-  
phosphate synthase, compared to an unmodified Coryneform bacterium.

48. (New) The process of Claim 47, wherein the otsA gene product is eliminated in  
the recombinant modified Coryneform bacterium.

49. (New) The process of Claim 47, wherein the expression of the otsA gene product  
is reduced at least 5% compared to an unmodified Coryneform bacterium.

50. (New) The process of Claim 47, wherein the expression of the otsA gene product  
is reduced at least 10% compared to an unmodified Coryneform bacterium.

51. (New) The process of Claim 47, wherein the expression of the otsA gene product  
is reduced at least 25% compared to an unmodified Coryneform bacterium.

**BEST AVAILABLE COPY**

52. (New) The process of Claim 47, wherein the expression of the otsA gene product is reduced at least 50% compared to an unmodified Coryneform bacterium.

53. (New) The process of Claim 47, wherein the expression of the otsA gene product is reduced at least 75% compared to an unmodified Coryneform bacterium.

54. (New) The process of Claim 46, wherein the recombinant modified Coryneform bacterium expresses a otsA gene product having reduced trehalose 6-phosphate synthase activity compared to the otsA gene product expressed in an unmodified Coryneform bacterium.

55. (New) The process of Claim 54, wherein the activity of the trehalose 6-phosphate synthase is reduced at least 5% compared to an unmodified Coryneform bacterium.

56. (New) The process of Claim 54, wherein the activity of the trehalose 6-phosphate synthase is reduced at least 10% compared to an unmodified Coryneform bacterium.

57. (New) The process of Claim 54, wherein the activity of the trehalose 6-phosphate synthase is reduced at least 25% compared to an unmodified Coryneform bacterium.

58. (New) The process of Claim 54, wherein the activity of the trehalose 6-phosphate synthase is reduced at least 50% compared to an unmodified Coryneform bacterium.

59. (New) The process of Claim 54, wherein the activity of the trehalose 6-phosphate synthase is reduced at least 75% compared to an unmodified Coryneform bacterium.

60. (New) The process of Claim 46, wherein said recombinant modified Coryneform bacteria is *Corynebacterium glutamicum*.

61. (New) The process of Claim 46, wherein said recombinant modified Coryneform bacterium is selected from the group consisting of *Corynebacterium acetooglutamicum*, *Corynebacterium acetoacidophilum*, *Corynebacterium thermoaminogenes*, and *Brevibacterium flavum*.

**BEST AVAILABLE COPY**

62. (New) The process of Claim 46, wherein said recombinant modified Coryneform bacterium further comprises an increased amount of the products of one or more of the following genes compared to the unmodified Coryneform bacterium: dapA which codes for dihydridopicolinate synthase, gap which codes for glyceraldehyde 3-phosphate dehydrogenase, eno which codes for enolase, tpi which codes for triose phosphate isomerase, pgk which codes for 3-phosphoglycerate kinase, zwf which codes for glucose 6-phosphate dehydrogenase, pyc which codes for pyruvate carboxylase, mqo which codes for malate-quinone oxidoreductase, lysC which codes for a feed-back resistant aspartate kinase, lysE which codes for lysine export, zwa1 which codes for the Zwa1 protein

63. (New) The process of Claim 62, wherein the dapA, gap, eno, tpi, pgk, zwf, pyc, mqo, lysC, lysE, and zwa1 genes are overexpressed in the recombinant modified Coryneform bacterium.

64. (New) The process of Claim 46, wherein said recombinant modified Coryneform bacterium further comprises a decreased amount of the products of one or more of the following genes compared to the unmodified Coryneform bacterium: pck gene codes for phosphoenol pyruvate carboxykinase, pgi which codes for glucose 6-phosphate isomerase, poxB which codes for pyruvate oxidase, zwa2 which codes for the Zwa2 protein, fda which codes for fructose 1,6-bisphosphate aldolase, hom which codes for homoserine dehydrogenase, thrB which codes for homoserine kinase and panD which codes for aspartate decarboxylase

65. (New) The process of Claim 46, wherein said otsA gene comprises a polynucleotide which hybridizes under stringent conditions to a complement of SEQ ID NO:1 and which encodes a protein having reduced trehalose 6-phosphate synthase activity compared to a protein encoded by SEQ ID NO:1, and wherein said stringent conditions comprise washing in 5X SSC at a temperature of 68°C.